

SEQUENCE LISTING



<110> French, Cynthia K.
Schneider, Patrick A.
Yamamoto, Karen K.

<120> Prostate Cancer-Specific Marker

<130> 107-206US-C

<140> 09/680,121

<141> 2000-10-04

<150> 60/041,246

<151> 1997-03-07

<150> 60/047,811

<151> 1997-05-15

<150> 09/036,315

<151> 1998-03-06

<150> 09/535,597

<151> 2000-03-27

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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<222> (151)..(1425)

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cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 174
Met Ala Pro Ile Thr Thr Ser Arg

gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt	222
Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe	
10 15 20	
ggc ctg gtc ttc aca gtc tct ctc ttt gca tgg atc tgc tgt cag aga	270
Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg	
25 30 35 40	
aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg	318
Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val	
45 50 55	
ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag	366
Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys	
60 65 70	
ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca	414
Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro	
75 80 85	
aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat	462
Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn	
90 95 100	
ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat	510
Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn	
105 110 115 120	
gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct	558
Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro	
125 130 135	
gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag	606
Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu	
140 145 150	
aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa	654
Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys	
155 160 165	
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Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp	
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Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro	

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205 210 215				
cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa				846
Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln				
220 225 230				
atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt				894
Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe				
235 240 245				
tca aga gat gat atc att ggg gaa gtt cta att cct ctc tcg gga att				942
Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile				
250 255 260				
gaa tta tct gaa gga aaa atg tta atg aat aga gag atc atc aag aga				990
Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg				
265 270 275 280				
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Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys				
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tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga				1086
Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg				
300 305 310				
cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa				1134
His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys				
315 320 325				
gtg aac ctg tac cat gcc aaa aag aga atc tcc aag aag aag act cat				1182
Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His				
330 335 340				
gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt				1230
Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe				
345 350 355 360				
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Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val				
365 370 375				
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Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val				

380

385

390

ttg ggt gca gca gca gaa gga act ggt gga gag cac tgg aaa gag atc 1374
 Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
 395 400 405

tgt gac tac ccc agg aga caa att gcc aag tgg cac gtg ctc tgt gat 1422
 Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
 410 415 420

ggt tagcatccta gccgtgagtt ggaacttaaa ggtttttact aggcaaggag 1475
 Gly
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aaatcttctt tctttctata ttggattgca agcttgggaa atcaagctac ctttttggtg 1535

ttgttggtgt tgctagaaat ggattgaatt agtagaccag aaagtaactt caaatgtgta 1595

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<213> Homo sapiens
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Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
35 40 45

Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
50 55 60

Glu Asn Leu Asn Ser Lys Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
65 70 75 80

Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
85 90 95

Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
100 105 110

Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
115 120 125

Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
130 135 140

Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
145 150 155 160

Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
165 170 175

Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
180 185 190

Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
195 200 205

Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr

210	215	220
Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe		
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Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu		
245	250	255
Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu		
260	265	270
Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg		
275	280	285
Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu		
290	295	300
Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser		
305	310	315 320
Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys		
325	330	335
Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala		
340	345	350
Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu		
355	360	365
Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg		
370	375	380
Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr		
385	390	395 400
Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile		
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Ala Lys Trp His Val Leu Cys Asp Gly		
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 <223> 5' oligo (109) Upper Primer

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 Phe Ala Trp Ile Cys Cys Gln Arg Arg Ser Ala Lys Ser Asn Lys Thr
 35 40 45
 Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
 50 55 60
 Glu Asn Leu Ser Ser Lys Lys Lys Phe Gly Gly Asp Asp Lys Ser Glu
 65 70 75 80
 Ala Lys Arg Lys Ala Ala Leu Pro Asn Leu Ser Leu His Leu Asp Leu

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Glu	Lys	Arg	Asp	Leu	Asn	Gly	Asn	Phe	Pro	Lys	Thr	Asn	Pro	Lys	Ala				
			100					105						110					
Gly	Ser	Ser	Ser	Asp	Leu	Glu	Asn	Val	Thr	Pro	Lys	Leu	Phe	Pro	Glu				
			115				120						125						
Thr	Glu	Lys	Glu	Ala	Val	Ser	Pro	Glu	Ser	Leu	Lys	Ser	Ser	Thr	Ser				
			130				135						140						
Leu	Thr	Ser	Glu	Glu	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Leu	Phe	Leu	Ser				
145					150					155					160				
Leu	Glu	Tyr	Asn	Phe	Glu	Lys	Lys	Ala	Phe	Val	Val	Asn	Ile	Lys	Glu				
				165					170					175					
Ala	Gln	Gly	Leu	Pro	Ala	Met	Asp	Glu	Gln	Ser	Met	Thr	Ser	Asp	Pro				
			180					185						190					
Tyr	Ile	Lys	Met	Thr	Ile	Leu	Pro	Glu	Lys	Lys	His	Lys	Val	Lys	Thr				
			195				200							205					
Arg	Val	Leu	Arg	Lys	Thr	Leu	Asp	Pro	Val	Phe	Asp	Glu	Thr	Phe	Thr				
			210				215							220					
Phe	Tyr	Gly	Val	Pro	Tyr	Pro	His	Ile	Gln	Glu	Leu	Ser	Leu	His	Phe				
225					230					235					240				
Thr	Val	Leu	Ser	Phe	Asp	Arg	Phe	Ser	Arg	Asp	Asp	Val	Ile	Gly	Glu				
				245					250					255					
Val	Leu	Val	Pro	Leu	Ser	Gly	Ile	Glu	Leu	Ser	Asp	Gly	Lys	Met	Leu				
			260					265						270					
Met	Thr	Arg	Glu	Ile	Ile	Lys	Arg	Asn	Ala	Lys	Lys	Ser	Ser	Gly	Arg				
			275				280							285					
Gly	Glu	Leu	Leu	Val	Ser	Leu	Cys	Tyr	Gln	Ser	Thr	Thr	Asn	Thr	Leu				
			290				295							300					
Thr	Val	Val	Val	Leu	Lys	Ala	Arg	His	Leu	Pro	Lys	Ser	Asp	Val	Ser				
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Gly	Leu	Ser	Asp	Pro	Tyr	Val	Lys	Val	Asn	Leu	Tyr	His	Ala	Lys	Lys				
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Arg	Ile	Ser	Lys	Lys	Lys	Thr	His	Val	Lys	Lys	Cys	Thr	Pro	Asn	Ala				

340	345	350
Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Ser Leu Glu		
355	360	365
Glu Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg		
370	375	380
Asn Glu Val Ile Gly Arg Leu Val Leu Gly Ala Thr Ala Glu Gly Ser		
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Gly Gly Gly His Trp Lys Glu Ile Cys Asp Phe Pro Arg Arg Gln Ile		
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Ala Lys Trp His Met Leu Cys Asp Gly		
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 <212> PRT
 <213> Homo sapiens

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 <223> PKC-C2 internal repeat (amino acid positions
 154-271)

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Arg Ile Tyr Leu Glu Ile Asn Val Lys Glu Asn Leu Leu Thr Val Gln
20 25 30
Ile Lys Glu Gly Arg Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser
35 40 45
Asp Pro Tyr Val Lys Val Lys Leu Ile Pro Asp Asp Lys Asp Gln Ser
50 55 60
Lys Lys Lys Thr Arg Thr Thr Lys Ala Cys Leu Asn Pro Val Trp Asn
65 70 75 80
Glu Thr Leu Thr Tyr Asp Leu Lys Pro Glu Asp Lys Asp Arg Arg Ile
85 90 95

Leu Ile Glu Val Trp Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met
100 105 110

Gly Ala Leu Ser Phe
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<210> 7
<211> 121
<212> PRT
<213> Homo sapiens

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<222> (1)..(121)
<223> Repro-PC-1.0 (PC-20) "B" internal repeat (amino
acid) positions 276-397

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Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu
1 5 10 15

Leu Ile Ser Leu Cys Tyr Gln Ser Thr Ile Asn Thr Leu Thr Val Val
20 25 30

Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser
35 40 45

Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser
50 55 60

Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn
65 70 75 80

Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser
85 90 95

Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val
100 105 110

Ile Gly Gln Leu Val Leu Gly Ala Ala
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<210> 8
<211> 115
<212> PRT
<213> rat

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<222> (1)..(115)

<223> synaptotagmin "B" internal repeat (amino acid
positions 268-383)

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Val Pro Thr Ala Gly Lys Leu Thr Val Val Ile Leu Glu Ala Lys Asn
20 25 30

Leu Lys Lys Met Asp Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile
35 40 45

His Leu Met Gln Asn Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile
50 55 60

Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu
65 70 75 80

Val Pro Phe Glu Gln Ile Gln Lys Val Gln Val Val Val Thr Val Leu
85 90 95

Asp Tyr Asp Lys Ile Gly Lys Asn Asp Ala Ile Gly Lys Val Phe Val
100 105 110

Gly Tyr Asn
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<210> 9

<211> 120

<212> PRT

<213> rat

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Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu Val Gly Ile Ile Gln
20 25 30

Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr
35 40 45

Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Phe Glu Thr Lys
50 55 60

Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu Gln Phe Thr Phe
65 70 75 80

Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu Val Met Ala Val
85 90 95

Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Phe Lys
100 105 110

Val Pro Met Asn Thr Val Asp Phe
115 120

<210> 10

<211> 113

<212> PRT

<213> Homo sapiens

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<222> (1)..(113)

<223> Repro=PC-1.0 (PC-20) "A" internal repeat amino
acid positions 150-263)

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Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro
20 25 30

Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr
35 40 45

Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys
50 55 60

Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro
65 70 75 80

Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe
85 90 95

Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu
100 105 110

Ser

<210> 11
<211> 9
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<223> residue 2=Asp, Glu, Ala, Ser or Thr

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<220>
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
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<210> 13
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<212> PRT
<213> Homo sapiens

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<210> 14
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<213> Homo sapiens

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<220>
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
1 5

<210> 15
<211> 9
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<213> Homo sapiens

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Cys, Gly, Asp or Glu

<220>
<223> residue 9=Lys, Arg or Tyr

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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<213> Homo sapiens

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Cys, Gly, Asp or Glu

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<223> residue 10=Lys, Arg or Tyr

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<223> residues 1,3-9=unknown

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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10

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<400> 17

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys

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<210> 18

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<213> Homo sapiens

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<223> residue 2=Thr or Val

<220>

<223> residues 1,3-10=unknown

<400> 18

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys

1

5

10

<210> 19

<211> 9

<212> PRT

<213> Homo sapiens

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<223> residue 2=Tyr, Phe or Trp

<220>

<223> residue 9=Phe, Ile, Trp, Met or Leu

<220>

<223> residues 1,3-8=unknown

<400> 19

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

<210> 20

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<223> residue 2=Tyr, Phe or Trp

<220>

<223> residues 1,3-10=unknown

<400> 20

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

10

<210> 21

<211> 31

<212> PRT

<213> Homo sapiens

<400> 21

Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe
1 5 10 15

Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln
20 25 30

<210> 22

<211> 34

<212> PRT

<213> Homo sapiens

<400> 22

Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val Leu
1 5 10 15

Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys Phe
20 25 30

Gly Ala

<210> 23

<211> 25

<212> PRT

<213> Homo sapiens

<400> 23

Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu Gly
1 5 10 15

Glu Lys Glu Ser Val Ser Pro Glu Ser
20 25

<210> 24

<211> 60

<212> PRT

<213> Homo sapiens

<400> 24

Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr
1 5 10 15

Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr

20

25

30

Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp
35 40 45

Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu
50 55 60

<210> 25

<211> 46

<212> PRT

<213> Homo sapiens

<400> 25

Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu Met Asn
1 5 10 15

Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu
20 25 30

Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
35 40 45

<210> 26

<211> 32

<212> PRT

<213> Homo sapiens

<400> 26

Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu
1 5 10 15

Val Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu
20 25 30

<210> 27

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> residue 5=Val or Ile

<400> 27

Ser Asp Pro Tyr Xaa Lys

1

5